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Siegerstetter, S-C., Petri, R. M., Magowan, E., Lawlor, P. G., Zebeli, Q., O'Connell, N., & Metzler-Zebeli, B. U. (2017). Fecal microbiota transplant from highly feed efficient donors shows little effects on age-related changes in feed efficiency-associated fecal microbiota in chickens. *Applied and Environmental Microbiology*, *84*(2), [e02330-17]. https://doi.org/10.1128/AEM.02330-17

Published in:
Applied and Environmental Microbiology

Document Version:
Peer reviewed version

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Running title: Fecal transplant and feed efficiency

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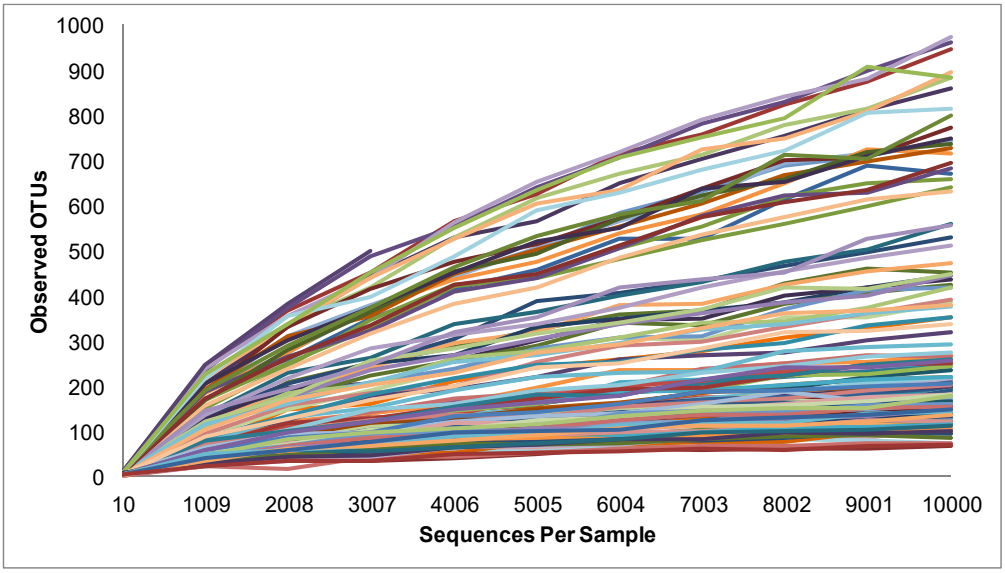
a



b

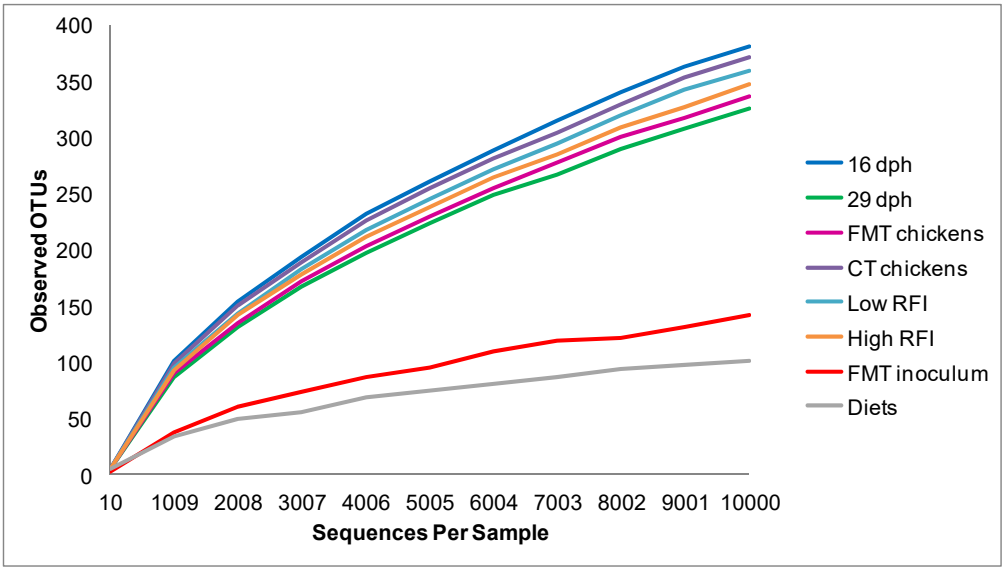


FIG S1 Rarefaction curves showing microbiota diversity based on Observed operational taxonomic units (OTUs): (a) separate for each of the fecal samples (n = 112), fecal microbiota transplant (FMT) (n = 8) and diet sample (n = 6); (b) summarized to day post-hatch (dph), FMT and control (CT) group, residual feed intake (RFI), FMT inoculum and diet sample means. Water samples were not included in the graphs due to their low number of sequencing reads/sample (162 and 180 sequences/sample, respectively).

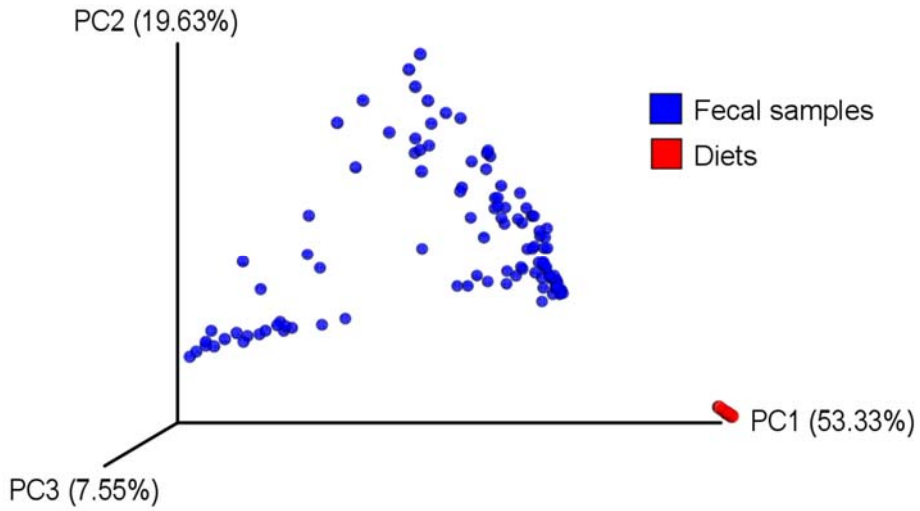


FIG S2 Principal coordinate analysis (PCoA) plot of weighted UniFrac analysis of fecal and diet samples. Fecal samples, *n* = 111, diet samples, *n* = 6. Rarefaction depth of 10,000 sequences per sample removed 1 sample from the dataset (male, low residual feed intake, control transplant, 16 day post-hatch).

TABLE S1 Descriptive statistics for the most abundant bacterial phyla in diet and water samples

Item	*n*	Mean	SE	Minimum	Maximum
Starter Diet					
Cyanobacteria	2	81.32	0.88	80.44	82.20
Proteobacteria	2	18.39	0.88	17.51	19.27
Firmicutes	2	0.24	0.02	0.22	0.25
Unclassified	2	0.03	0.01	0.02	0.04
Actinobacteria	2	0.02	0.004	0.01	0.02
Tenericutes	2	0.002	0.002	0	0.003
Spirochaetes	2	0.002	0.002	0	0.003
TM7	2	0.002	0.002	0	0.003
Grower Diet					
Cyanobacteria	2	76.22	2.81	73.42	79.03
Proteobacteria	2	23.50	2.76	20.74	26.26
Firmicutes	2	0.21	0.01	0.20	0.22
Actinobacteria	2	0.03	0.03	0.004	0.06
Unclassified	2	0.03	0.02	0.01	0.04
Bacteroidetes	2	0.004	0.004	0	0.008
Tenericutes	2	0.002	0.002	0	0.004
Finisher Diet					
Cyanobacteria	2	80.02	3.06	76.96	83.07
Proteobacteria	2	19.64	3.10	16.54	22.74
Firmicutes	2	0.27	0.05	0.22	0.32
Unclassified	2	0.03	0.01	0.02	0.04
Actinobacteria	2	0.02	0.003	0.02	0.02
Bacteroidetes	2	0.01	0.01	0	0.03
Spirochaetes	2	0.004	0.0001	0.004	0.004
Water					
Firmicutes	2	77.99	4.10	73.89	82.10
Proteobacteria	2	18.80	3.98	14.81	22.78
Cyanobacteria	2	1.23	1.23	0	2.47
Actinobacteria	2	0.59	0.03	0.56	0.62
Tenericutes	2	0.56	0.56	0	1.11
Unclassified	2	0.28	0.28	0	0.56
Bacteroidetes	2	0.28	0.28	0	0.56
Spirochaetes	2	0.28	0.28	0	0.56

TABLE S2 Descriptive statistics for the most abundant operational taxonomic units (OTUs) in diet and water samples

Item	Taxonomy (Genus)[a]	*n*	Mean	SE	Minimum	Maximum
Starter Diet						
OTU14	Unclassified *Streptophyta*	2	31.54	6.52	25.01	38.06
OTU17	Unclassified *Streptophyta*	2	23.17	3.54	19.64	26.71
OTU25	Unclassified *Streptophyta*	2	14.55	2.18	12.37	16.73
OTU38	Unclassified mitochondria	2	8.43	0.33	8.11	8.76
OTU57	Unclassified *Streptophyta*	2	5.60	0.94	4.66	6.54
OTU61	Unclassified mitochondria	2	4.45	0.26	4.19	4.71
OTU87	Unclassified *Streptophyta*	2	3.30	0.68	2.62	3.98
OTU122	Unclassified mitochondria	2	1.90	0.24	1.66	2.15
OTU142	Unclassified *Streptophyta*	2	1.71	0.21	1.50	1.91
OTU125	Unclassified mitochondria	2	1.52	0.15	1.36	1.67
OTU375	Unclassified *Streptophyta*	2	0.38	0.04	0.34	0.42
OTU381	*Erwinia*	2	0.24	0.01	0.23	0.25
OTU557	Unclassified *Streptophyta*	2	0.23	0.04	0.19	0.27
OTU508	Unclassified *Streptophyta*	2	0.23	0.03	0.20	0.26
OTU53	Unclassified *Enterobacteriaceae*	2	0.23	0.09	0.14	0.31
OTU643	*Stenotrophomonas*	2	0.13	0.12	0.01	0.25
OTU752	Unclassified mitochondria	2	0.11	0.006	0.10	0.11
OTU621	*Vibrio*	2	0.09	0.002	0.09	0.09
OTU1	Unclassified *Enterobacteriaceae*	2	0.05	0.007	0.04	0.06
OTU2	*Lactobacillus*	2	0.02	0.007	0.02	0.03
OTU3	*Turicibacter*	2	0.02	0.007	0.01	0.03
OTU5	*Lactobacillus*	2	0.01	0.002	0.008	0.01
OTU8	*Lactobacillus*	2	0.007	0.002	0.004	0.009
OTU20	*Lactobacillus*	2	0.007	0.002	0.004	0.009
OTU127	*Sphingomonas*	2	0.006	0.003	0.003	0.008
OTU245	Unclassified *Comamonadaceae*	2	0.005	0.001	0.004	0.006
OTU32	Unclassified *Clostridiales*	2	0.004	0.001	0.003	0.004
OTU7	*Lactobacillus*	2	0.004	0.001	0.003	0.004
OTU4	Unclassified *Ruminococcaceae*	2	0.003	0.003	0	0.006
OTU107	Unclassified *Ruminococcaceae*	2	0.003	0.003	0	0.006
OTU214	Unclassified *Sinobacteraceae*	2	0.002	0.002	0	0.004
OTU72	Unclassified *Ruminococcaceae*	2	0.002	0.002	0	0.003
OTU105	Unclassified family 0319-6G20	2	0.002	0.002	0	0.003
OTU63	Unclassified *Ruminococcaceae*	2	0.002	0.002	0	0.003
OTU10	Unclassified *Clostridiales*	2	0.002	0.002	0	0.003
OTU31	Unclassified *Lachnospiraceae*	2	0.002	0.002	0	0.003

OTU15	Unclassified *Ruminococcaceae*	2	0.002	0.002	0	0.003
OTU33	Unclassified *Enterobacteriaceae*	2	0.002	0.002	0	0.003
Grower Diet						
OTU14	Unclassified *Streptophyta*	2	29.18	2.16	27.01	31.34
OTU17	Unclassified *Streptophyta*	2	21.93	0.89	21.04	22.82
OTU25	Unclassified *Streptophyta*	2	13.83	0.31	13.52	14.14
OTU38	Unclassified mitochondria	2	10.39	0.39	10.01	10.78
OTU61	Unclassified mitochondria	2	6.70	1.95	4.75	8.64
OTU57	Unclassified *Streptophyta*	2	5.52	0.16	5.36	5.67
OTU87	Unclassified *Streptophyta*	2	3.22	0.11	3.12	3.33
OTU125	Unclassified mitochondria	2	2.44	0.84	1.60	3.28
OTU122	Unclassified mitochondria	2	2.02	0.003	2.02	2.02
OTU142	Unclassified *Streptophyta*	2	1.38	0.03	1.36	1.41
OTU381	*Erwinia*	2	0.33	0.15	0.17	0.48
OTU375	Unclassified *Streptophyta*	2	0.28	0.03	0.25	0.31
OTU508	Unclassified *Streptophyta*	2	0.24	0.01	0.23	0.25
OTU752	Unclassified mitochondria	2	0.14	0.02	0.12	0.16
OTU557	Unclassified *Streptophyta*	2	0.12	0.01	0.11	0.13
OTU621	*Vibrio*	2	0.10	0.02	0.08	0.12
OTU53	Unclassified *Enterobacteriaceae*	2	0.09	0.01	0.08	0.10
OTU1	Unclassified *Enterobacteriaceae*	2	0.07	0.004	0.06	0.07
OTU7	*Lactobacillus*	2	0.04	0.04	0.004	0.08
OTU643	*Stenotrophomonas*	2	0.03	0.02	0.009	0.06
OTU3	*Turicibacter*	2	0.02	0.007	0.01	0.03
OTU26	Unclassified *Clostridiales*	2	0.007	0.002	0.004	0.009
OTU127	*Sphingomonas*	2	0.006	0.002	0.004	0.008
OTU5	*Lactobacillus*	2	0.004	0.0002	0.004	0.004
OTU2	*Lactobacillus*	2	0.004	0.0002	0.004	0.004
OTU105	Unclassified family 0319-6G20	2	0.004	0.004	0	0.008
OTU110	*Phenylobacterium*	2	0.004	0.004	0	0.008
OTU8	*Lactobacillus*	2	0.002	0.002	0	0.004
OTU172	*Slackia*	2	0.002	0.002	0	0.004
OTU20	*Lactobacillus*	2	0.002	0.002	0	0.004
OTU214	Unclassified *Sinobacteraceae*	2	0.002	0.002	0	0.004
OTU19	*Ruminococcus*	2	0.002	0.002	0	0.004
OTU245	Unclassified *Comamonadaceae*	2	0.002	0.002	0	0.004
OTU29	Unclassified *Clostridiales*	2	0.002	0.002	0	0.004
Finisher Diet						
OTU14	Unclassified *Streptophyta*	2	33.76	0.07	33.69	33.83

OTU17	Unclassified *Streptophyta*	2	21.14	1.80	19.34	22.94
OTU25	Unclassified *Streptophyta*	2	13.38	0.67	12.71	14.05
OTU38	Unclassified mitochondria	2	9.39	1.05	8.35	10.44
OTU57	Unclassified *Streptophyta*	2	5.85	0.16	5.70	6.01
OTU61	Unclassified mitochondria	2	4.53	0.42	4.12	4.95
OTU87	Unclassified *Streptophyta*	2	2.69	0.30	2.39	2.99
OTU142	Unclassified *Streptophyta*	2	1.82	0.15	1.66	1.97
OTU122	Unclassified mitochondria	2	1.72	0.35	1.37	2.06
OTU125	Unclassified mitochondria	2	1.66	0.14	1.52	1.79
OTU53	Unclassified *Enterobacteriaceae*	2	0.54	0.46	0.07	1.00
OTU375	Unclassified *Streptophyta*	2	0.39	0.002	0.39	0.39
OTU621	*Vibrio*	2	0.28	0.26	0.02	0.54
OTU381	*Erwinia*	2	0.22	0.04	0.19	0.26
OTU557	Unclassified *Streptophyta*	2	0.22	0.03	0.19	0.25
OTU643	*Stenotrophomonas*	2	0.20	0.20	0.004	0.40
OTU508	Unclassified *Streptophyta*	2	0.19	0.007	0.19	0.20
OTU752	Unclassified mitochondria	2	0.10	0.002	0.10	0.11
OTU1	Unclassified *Enterobacteriaceae*	2	0.04	0.009	0.03	0.05
OTU3	*Turicibacter*	2	0.03	0.01	0.02	0.04
OTU9	Unclassified *Clostridiales*	2	0.02	0.008	0.01	0.03
OTU2	*Lactobacillus*	2	0.01	0.005	0.004	0.02
OTU5	*Lactobacillus*	2	0.009	0.005	0.004	0.01
OTU32	Unclassified *Clostridiales*	2	0.008	0.004	0.004	0.01
OTU105	Unclassified family 0319-6G20	2	0.008	0.004	0.004	0.01
OTU8	*Lactobacillus*	2	0.007	0.004	0.004	0.01
OTU31	Unclassified *Lachnospiraceae*	2	0.006	0.006	0	0.01
OTU7	*Lactobacillus*	2	0.006	0.006	0	0.01
OTU214	Unclassified *Sinobacteraceae*	2	0.006	0.002	0.004	0.008
OTU19	*Ruminococcus*	2	0.006	0.002	0.004	0.007
OTU127	*Sphingomonas*	2	0.005	0.005	0	0.01
OTU26	Unclassified *Clostridiales*	2	0.004	0.0001	0.004	0.004
OTU20	*Lactobacillus*	2	0.004	0.004	0	0.007
OTU232	Unclassified family 0319-6G20	2	0.004	0.004	0	0.007
OTU4	Unclassified *Ruminococcaceae*	2	0.002	0.002	0	0.004
OTU63	Unclassified *Ruminococcaceae*	2	0.002	0.002	0	0.004
OTU15	Unclassified *Ruminococcaceae*	2	0.002	0.002	0	0.004
OTU75	Unclassified *Clostridiales*	2	0.002	0.002	0	0.004
OTU364	Unclassified *Peptostreptococcaceae*	2	0.002	0.002	0	0.004
OTU29	Unclassified *Clostridiales*	2	0.002	0.002	0	0.004
OTU22	*Turicibacter*	2	0.002	0.002	0	0.004
OTU411	Unclassified *Clostridiales*	2	0.002	0.002	0	0.004

Water						
OTU9	Unclassified *Clostridiales*	2	14.20	14.20	0	28.40
OTU1	Unclassified *Enterobacteriaceae*	2	12.22	1.11	11.11	13.33
OTU32	Unclassified *Clostridiales*	2	9.17	7.50	1.67	16.67
OTU11	Unclassified *Clostridiales*	2	4.72	4.72	0.00	9.44
OTU5	*Lactobacillus*	2	3.73	1.27	2.47	5.00
OTU4	Unclassified *Ruminococcaceae*	2	2.90	0.43	2.47	3.33
OTU26	Unclassified *Clostridiales*	2	2.81	2.19	0.62	5.00
OTU72	Unclassified *Ruminococcaceae*	2	2.59	0.74	1.85	3.33
OTU3	*Turicibacter*	2	2.56	1.33	1.23	3.89
OTU8	*Lactobacillus*	2	2.28	1.05	1.23	3.33
OTU2	*Lactobacillus*	2	1.51	0.96	0.56	2.47
OTU105	Unclassified family 0319-6G20	2	1.48	0.37	1.11	1.85
OTU63	Unclassified *Ruminococcaceae*	2	1.20	0.65	0.56	1.85
OTU39	Unclassified *Lachnospiraceae*	2	1.17	0.06	1.11	1.23
OTU20	*Lactobacillus*	2	1.11	1.11	0	2.22
OTU10	Unclassified *Clostridiales*	2	1.11	1.11	0	2.22
OTU28	Unclassified *Clostridiales*	2	1.11	1.11	0	2.22
OTU251	Unclassified *Clostridiales*	2	1.11	1.11	0	2.22
OTU182	Unclassified *Clostridiales*	2	0.93	0.93	0	1.85
OTU225	Unclassified *Clostridiales*	2	0.93	0.93	0	1.85
OTU79	*Ruminococcus*	2	0.90	0.34	0.56	1.23
OTU65	*Ruminococcus*	2	0.86	0.25	0.62	1.11
OTU94	Unclassified *Ruminococcaceae*	2	0.86	0.25	0.62	1.11
OTU214	Unclassified *Sinobacteraceae*	2	0.83	0.83	0	1.67
OTU19	*Ruminococcus*	2	0.83	0.83	0	1.67
OTU31	Unclassified *Lachnospiraceae*	2	0.83	0.83	0	1.67
OTU245	Unclassified *Comamonadaceae*	2	0.83	0.83	0	1.67
OTU15	Unclassified *Ruminococcaceae*	2	0.62	0.62	0	1.23
OTU35	Unclassified *Clostridiales*	2	0.62	0.62	0	1.23
OTU232	Unclassified family 0319-6G20	2	0.59	0.03	0.56	0.62
OTU172	*Slackia*	2	0.59	0.03	0.56	0.62
OTU75	Unclassified *Clostridiales*	2	0.59	0.03	0.56	0.62
OTU48	Unclassified *Ruminococcaceae*	2	0.59	0.03	0.56	0.62
OTU74	Unclassified *Ruminococcaceae*	2	0.59	0.03	0.56	0.62
OTU342	*Ruminococcus*	2	0.59	0.03	0.56	0.62
OTU360	Unclassified *Lachnospiraceae*	2	0.59	0.03	0.56	0.62
OTU127	*Sphingomonas*	2	0.56	0.56	0	1.11
OTU29	Unclassified *Clostridiales*	2	0.56	0.56	0	1.11
OTU22	*Turicibacter*	2	0.56	0.56	0	1.11

OTU165	Unclassified *Lachnospiraceae*	2	0.56	0.56	0	1.11
OTU363	Unclassified *RF39*	2	0.56	0.56	0	1.11
OTU14	Unclassified *Streptophyta*	2	0.31	0.31	0	0.62
OTU17	Unclassified *Streptophyta*	2	0.31	0.31	0	0.62
OTU25	Unclassified *Streptophyta*	2	0.31	0.31	0	0.62
OTU57	Unclassified *Streptophyta*	2	0.31	0.31	0	0.62
OTU7	*Lactobacillus*	2	0.31	0.31	0	0.62
OTU110	*Phenylobacterium*	2	0.31	0.31	0	0.62
OTU107	Unclassified *Ruminococcaceae*	2	0.31	0.31	0	0.62
OTU364	Unclassified *Peptostreptococcaceae*	2	0.31	0.31	0	0.62
OTU411	Unclassified *Clostridiales*	2	0.31	0.31	0	0.62
OTU33	Unclassified *Enterobacteriaceae*	2	0.31	0.31	0	0.62

39 [a]Taxonomic classification based on the 13_8 Greengenes default database in Qiime (version 1.9.1).

TABLE S3 Differences in relative abundance (%) of most abundant operational taxonomic units (OTUs) in feces at 16 and 29 days post-hatch (dph) in low and high residual feed intake (RFI) broiler chickens receiving either a fecal microbiota transplant (FMT) or a control transplant (CT)

		16 dph				29 dph									
		FMT		CT		FMT		CT			*P* value				
Item	Taxonomy (Genus)[a,b]	Low RFI	High RFI	Low RFI	High RFI	Low RFI	High RFI	Low RFI	High RFI	SEM	T[c]	FMT	RFI	FMT×RFI	T×FMT×RFI
OTU1	*Escherichia/Shigella*	29.79	52.21	30.47	41.94	51.47	49.59	47.33	52.14	7.638	0.032	0.619	0.105	0.850	0.401
OTU2	*Lactobacillus*	11.72	8.43	10.24	6.17	5.22	5.31	4.14	2.05	2.766	0.020	0.280	0.211	0.691	0.929
OTU3	*Turicibacter*	0.99	1.76	0.37	0.20	12.11	12.02	8.42	5.78	3.015	<0.001	0.164	0.804	0.686	0.793
OTU7	*Lactobacillus*	4.68	5.39	7.63	8.06	0.66	0.96	1.96	0.85	1.904	<0.001	0.237	0.955	0.768	0.809
OTU4	*Eubacterium*	5.74	2.19	3.88	6.02	0.52	1.37	1.70	1.98	1.600	0.001	0.483	0.958	0.339	0.325
OTU6	*Escherichia/Shigella*	1.71	2.96	1.79	2.37	3.15	3.01	2.85	3.19	0.435	0.007	0.628	0.114	0.881	0.430
OTU5	*Lactobacillus*	4.63	3.27	4.95	1.65	2.16	0.86	1.48	0.56	1.393	0.026	0.546	0.073	0.682	0.880
OTU8	*Lactobacillus*	3.23	2.40	3.75	1.14	1.54	0.58	1.11	0.40	1.056	0.032	0.636	0.079	0.590	0.863
OTU16	*Anaerobacterium*	0.83	0.22	2.15	0.86	0.23	0.74	1.67	1.50	0.773	0.968	0.086	0.519	0.568	0.731
OTU15	*Eubacterium*	1.43	0.52	0.98	1.42	0.13	0.39	0.42	0.47	0.391	0.002	0.530	0.902	0.383	0.295
OTU22	*Turicibacter*	0.09	0.16	0.03	0.02	1.25	1.16	0.84	0.55	0.288	<0.001	0.141	0.699	0.734	0.708
OTU26	*Gracilibacter*	0.31	0.05	0.32	0.15	0.49	0.20	0.67	1.18	0.331	0.065	0.196	0.824	0.367	0.480
OTU28	*Anaerobacterium*	0.28	0.11	0.76	0.36	0.21	0.31	0.74	0.41	0.220	0.783	0.055	0.250	0.347	0.910
OTU13	*Acinetobacter*	0.12	0.06	0.008	0.04	0.17	1.27	0.43	0.98	0.394	0.020	0.886	0.158	0.693	0.435
OTU21	*Lactobacillus*	0.64	0.40	0.69	0.21	0.32	0.13	0.22	0.08	0.196	0.048	0.574	0.051	0.703	0.868
OTU34	*Turicibacter*	0.03	0.04	0.006	0.007	0.66	0.37	0.60	0.58	0.137	<0.001	0.789	0.409	0.474	0.712
OTU46	*Lactobacillus*	0.34	0.38	0.54	0.61	0.05	0.09	0.16	0.07	0.142	<0.001	0.238	0.899	0.802	0.776
OTU33	*Escherichia/Shigella*	0.08	0.09	0.05	0.08	0.57	0.39	0.51	0.44	0.100	<0.001	0.842	0.446	0.600	0.786
OTU27	*Lactobacillus*	0.52	0.34	0.40	0.27	0.19	0.22	0.16	0.08	0.117	0.014	0.262	0.270	0.835	0.851
OTU30	*Lactobacillus*	0.46	0.33	0.51	0.17	0.20	0.08	0.13	0.04	0.138	0.016	0.544	0.076	0.640	0.854

OTU35	*Eisenbergiella*	0.34	0.18	0.19	0.81	0.02	0.04	0.02	0.27	0.167	0.009	0.176	0.172	0.055	0.562
OTU58	*Anaerobacterium*	0.17	0.04	0.50	0.15	0.05	0.18	0.39	0.32	0.174	0.873	0.090	0.444	0.439	0.687
OTU44	*Turicibacter*	0.04	0.07	0.01	0.007	0.52	0.49	0.36	0.25	0.123	<0.001	0.164	0.736	0.745	0.794
OTU31	[*Ruminococcus*]	0.60	0.12	0.26	0.33	0.06	0.05	0.07	0.09	0.126	0.003	0.840	0.310	0.132	0.241
OTU32	*Saccharofermentans*	0.50	0.11	0.15	0.29	0.13	0.04	0.13	0.15	0.125	0.106	0.858	0.337	0.062	0.525
OTU56	*Anaerobacterium*	0.06	0.04	0.20	0.19	0.12	0.09	0.35	0.15	0.093	0.395	0.040	0.352	0.549	0.765
OTU42	*Lactobacillus*	0.28	0.20	0.29	0.10	0.14	0.06	0.09	0.04	0.083	0.034	0.500	0.076	0.740	0.883
OTU47	*Lactobacillus*	0.27	0.10	0.31	0.10	0.11	0.11	0.08	0.03	0.077	0.045	0.724	0.049	0.693	0.469
OTU39	[*Clostridium*]	0.29	0.07	0.18	0.25	0.04	0.15	0.04	0.07	0.069	0.013	0.977	0.959	0.307	0.113
OTU43	*Lactobacillus*	0.24	0.09	0.32	0.10	0.12	0.09	0.07	0.02	0.076	0.050	0.917	0.039	0.631	0.490
OTU65	[*Clostridium*]	0.09	0.06	0.04	0.14	0.07	0.15	0.17	0.29	0.068	0.097	0.153	0.153	0.325	0.633
OTU80	*Acetivibrio*	0.14	0.05	0.14	0.11	0.03	0.07	0.15	0.19	0.057	0.999	0.070	0.765	0.777	0.389
OTU81	*Anaerobacterium*	0.24	0.01	0.13	0.07	0.17	0.05	0.13	0.06	0.088	0.910	0.787	0.050	0.320	0.952
OTU89	*Hespellia*	0.14	0.02	0.16	0.28	0.05	0.04	0.03	0.07	0.067	0.030	0.126	0.854	0.131	0.398
OTU53	*Klebsiella*	0.07	0.26	0.04	0.14	0.03	0.07	0.07	0.10	0.071	0.265	0.694	0.072	0.627	0.494
OTU18	*Klebsiella*	0.08	0.03	0.16	0.19	0.06	0.03	0.07	0.11	0.057	0.263	0.034	0.926	0.334	0.840
OTU68	*Flintibacter*	0.14	0.03	0.13	0.21	0.04	0.05	0.04	0.10	0.050	0.041	0.161	0.794	0.137	0.502
OTU51	*Lactobacillus*	0.19	0.06	0.17	0.05	0.11	0.06	0.05	0.03	0.057	0.233	0.457	0.043	0.838	0.779
OTU74	*Eubacterium*	0.19	0.08	0.11	0.17	0.02	0.05	0.05	0.06	0.052	0.004	0.753	0.956	0.391	0.405
OTU71	*Lactobacillus*	0.13	0.10	0.13	0.09	0.06	0.07	0.05	0.03	0.033	0.018	0.487	0.323	0.663	0.929
OTU95	*Escherichia/Shigella*	0.01	0.01	0.004	0.004	0.17	0.10	0.16	0.15	0.035	<0.001	0.800	0.386	0.553	0.741
OTU119	*Anaerobacterium*	0.05	0.02	0.17	0.05	0.03	0.06	0.10	0.11	0.046	0.963	0.057	0.426	0.485	0.446
OTU96	*Pseudoflavonifractor*	0.11	0.03	0.08	0.13	0.02	0.03	0.04	0.11	0.036	0.096	0.145	0.590	0.081	0.432
OTU67	*Lactobacillus*	0.13	0.05	0.13	0.04	0.08	0.05	0.04	0.02	0.043	0.214	0.477	0.037	0.964	0.789
OTU84	*Flintibacter*	0.11	0.02	0.09	0.14	0.03	0.04	0.03	0.08	0.034	0.040	0.202	0.839	0.130	0.410
OTU129	*Lactobacillus*	0.10	0.04	0.18	0.08	0.01	0.05	0.04	0.007	0.048	0.034	0.482	0.271	0.444	0.455

OTU107	*Flintibacter*	0.16	0.006	0.04	0.10	0.03	0.05	0.06	0.07	0.038	0.386	0.771	0.583	0.090	0.087
OTU103	*Turicibacter*	0.007	0.01	0.003	0.003	0.15	0.08	0.14	0.12	0.029	<0.001	0.888	0.310	0.595	0.650
OTU113	*Comamonas*	0.13	0.26	0.02	0.09	0.001	0.003	0.003	0.006	0.050	0.001	0.055	0.168	0.729	0.133
OTU132	*Lactobacillus*	0.09	0.04	0.18	0.07	0.01	0.06	0.03	0.008	0.045	0.029	0.533	0.326	0.383	0.325
OTU93	*Lactobacillus*	0.11	0.07	0.08	0.06	0.05	0.04	0.03	0.02	0.023	0.011	0.242	0.163	0.927	0.973
OTU117	[*Clostridium*]	0.15	0.002	0.04	0.08	0.03	0.04	0.06	0.05	0.035	0.346	0.988	0.334	0.102	0.070
OTU130	*Anaerobacterium*	0.03	0.01	0.08	0.07	0.04	0.04	0.11	0.06	0.035	0.468	0.087	0.421	0.724	0.919
OTU150	*Oscillibacter*	0.13	0.01	0.13	0.08	0.02	0.02	0.03	0.03	0.048	0.063	0.506	0.239	0.596	0.621
OTU77	*Oscillibacter*	0.10	0.06	0.05	0.12	0.01	0.07	0.01	0.02	0.032	0.023	0.785	0.312	0.525	0.281
OTU98	*Lactobacillus*	0.09	0.07	0.10	0.03	0.05	0.02	0.04	0.01	0.028	0.044	0.534	0.074	0.515	0.872

Data are presented as least-square means and pooled SEM.

Low RFI FMT females, *n* = 8/time point; low RFI FMT males, *n* = 7/time point; high RFI FMT females, *n* = 7/time point; high RFI FMT males, *n* = 6/time point; low RFI CT females, *n* = 7/time point; low RFI CT males, *n* = 7/time point; high RFI CT females, *n* = 7/time point; high RFI CT males, *n* = 7/time point.

[a]Taxonomic classification based on the National Center for Biotechnology Information (NCBI) nucleotide database using Blastn for taxonomic classification and the database limited to the 16S rRNA target (https://blast.ncbi.nlm.nih.gov/).

[b]Sequences not distinguishable between *Escherichia* and *Shigella*.

[c]T, time point.

49 **TABLE S4** BLAST search results for selected operational taxonomic units (OTUs)[a,b]

OTU	Blast hit (16S NCBI database)	Accession Number	Percent idendity
OTU1	*Escherichia coli* strain JCM 1649	NR_112558.1	100
	Shigella flexneri strain ATCC 29903	NR_026331.1	100
OTU2	*Lactobacillus salivarius* strain HO 66	NR_028725.2	99
OTU3	*Turicibacter sanguinis* strain MOL361	NR_028816.1	99
OTU4	*Eubacterium desmolans* strain ATCC 43058	NR_044644.2	98
OTU5	*Lactobacillus crispatus* strain DSM 20584	NR_119274.1	99
OTU6	*Escherichia coli* strain JCM 1649	NR_112558.1	99
	Shigella flexneri strain ATCC 29903	NR_026331.1	99
OTU7	*Lactobacillus johnsonii* strain CIP 103620	NR_117574.1	99
OTU8	*Lactobacillus crispatus* strain DSM 20584	NR_119274.1	99
OTU13	*Acinetobacter bereziniae* strain ATCC 17924	NR_117625.1	99
OTU15	*Eubacterium desmolans* strain ATCC 43058	NR_044644.2	98
OTU16	*Anaerobacterium chartisolvens* strain T-1-35	NR_125464.1	88
OTU18	*Klebsiella variicola* strain F2R9	NR_025635.1	99
OTU21	*Lactobacillus crispatus* strain DSM 20584	NR_119274.1	99
OTU22	*Turicibacter sanguinis* strain MOL361	NR_028816.1	99
OTU24	*Romboutsia timonensis* strain DR1	NR_144740.1	99
OTU26	*Gracilibacter thermotolerans* strain JW/YJL-S1	NR_115693.1	87
OTU27	*Lactobacillus salivarius* strain HO 66	NR_028725.2	99
OTU28	*Anaerobacterium chartisolvens* strain T-1-35	NR_125464.1	89
OTU29	*Anaerobacterium chartisolvens* strain T-1-35	NR_125464.1	88
OTU30	*Lactobacillus crispatus* strain DSM 20584	NR_119274.1	99
OTU31	[*Ruminococcus*] *torques* strain VPI B2-51	NR_036777.1	97
OTU32	*Saccharofermentans acetigenes* strain P6	NR_115340.1	87
OTU33	*Escherichia coli* strain JCM 1649	NR_112558.1	99
	Shigella flexneri strain ATCC 29903	NR_026331.1	99
OTU34	*Turicibacter sanguinis* strain MOL361	NR_028816.1	92
OTU35	*Eisenbergiella massiliensis* strain AT11	NR_144731.1	95
OTU39	[*Clostridium*] *saccharolyticum* strain WM1	NR_102852.1	96
OTU42	*Lactobacillus crispatus* strain DSM 20584	NR_119274.1	99
OTU43	*Lactobacillus salivarius* strain HO 66	NR_028725.2	96
OTU44	*Turicibacter sanguinis strain* MOL361	NR_028816.1	99
OTU46	*Lactobacillus johnsonii* strain CIP 103620	NR_117574.1	99
OTU47	*Lactobacillus salivarius* strain HO 66	NR_028725.2	97
OTU48	*Negativibacillus massiliensis* strain Marseille-P3213	NR_147378.1	93
OTU50	*Gracilibacter thermotolerans* strain JW/YJL-S1	NR_115693.1	87
OTU51	*Lactobacillus crispatus* strain DSM 20584	NR_119274.1	96
OTU52	[*Clostridium*] *leptum* strain DSM 753	NR_114789.1	97

OTU53	*Klebsiella oxytoca* strain NBRC 102593	NR_114152.1	99
OTU55	*Clostridium disporicum* strain DS1	NR_026491.1	100
OTU56	*Anaerobacterium chartisolvens* strain T-1-35	NR_125464.1	88
OTU58	*Anaerobacterium chartisolvens* strain T-1-35	NR_125464.1	88
OTU60	[*Clostridium*] *leptum* strain DSM 753	NR_114789.1	94
OTU64	*Hespellia stercorisuis* strain PC18	NR_025207.1	88
OTU65	[*Clostridium*] *leptum* strain DSM 753	NR_114789.1	92
OTU67	*Lactobacillus crispatus* strain DSM 20584	NR_119274.1	97
OTU68	*Flintibacter butyricus* strain BLS21	NR_144611.1	98
OTU70	*Negativibacillus massiliensis* strain Marseille-P3213	NR_147378.1	93
OTU71	*Lactobacillus salivarius* strain HO 66	NR_028725.2	99
OTU74	*Eubacterium desmolans* strain ATCC 43058	NR_044644.2	98
OTU75	*Eisenbergiella massiliensis* strain AT11	NR_144731.1	95
OTU77	*Oscillibacter ruminantium* strain GH1	NR_118156.1	95
OTU79	[*Clostridium*] *leptum* strain DSM 753	NR_114789.1	95
OTU80	*Acetivibrio cellulolyticus* strain CD2	NR_025917.1	95
OTU81	*Anaerobacterium chartisolvens* strain T-1-35	NR_125464.1	89
OTU83	*Anaerotruncus colihominis* strain WAL 14565	NR_027558.1	99
OTU84	*Flintibacter butyricus* strain BLS21	NR_144611.1	98
OTU88	*Gracilibacter thermotolerans* strain JW/YJL-S1	NR_115693.1	86
OTU89	*Hespellia porcina* strain PC80	NR_025206.1	96
OTU93	*Lactobacillus salivarius* strain HO 66	NR_028725.2	98
OTU95	*Escherichia coli* strain JCM 1649	NR_112558.1	92
	Shigella flexneri strain ATCC 29903	NR_026331.1	92
OTU96	*Pseudoflavonifractor phocaeensis* strain Marseille-P3064	NR_147370.1	96
OTU97	*Oscillibacter ruminantium* strain GH1	NR_118156.1	95
OTU98	*Lactobacillus crispatus* strain DSM 20584	NR_119274.1	99
OTU103	*Turicibacter sanguinis* strain MOL361	NR_028816.1	91
OTU107	*Flintibacter butyricus* strain BLS21	NR_144611.1	94
OTU113	*Comamonas thiooxydans* strain S23	NR_115741.1	99
OTU117	[*Clostridium*] *viride* strain T2-7	NR_026204.1	92
OTU119	*Anaerobacterium chartisolvens* strain T-1-35	NR_125464.1	87
OTU129	*Lactobacillus johnsonii* strain CIP 103620	NR_117574.1	97
OTU130	*Anaerobacterium chartisolvens* strain T-1-35	NR_125464.1	88
OTU132	*Lactobacillus johnsonii* strain CIP 103620	NR_117574.1	95
OTU150	*Oscillibacter ruminantium* strain GH1	NR_118156.1	95

[a]BLAST search was performed for the most abundant OTUs in the fecal microbiota transplant as well as for the OTUs in feces differently affected by time point, fecal microbiota transplant or residual feed intake.

[b]National Center for Biotechnology Information (NCBI) nucleotide database (https://blast.ncbi.nlm.nih.gov/); last accessed 12/10/2017.

TABLE S5 Dietary ingredients and chemical composition of diets (on as-fed basis)

Item	Starter 1-8 days post-hatch	Grower 9-20 days post-hatch	Finisher 21-30 days post-hatch
Ingredient (%)			
Corn	56.392	61.772	63.928
Soybean meal	37.032	31.432	29.068
Soybean oil	2.284	2.676	3.412
Monocalcium phosphate	1.460	1.412	1.240
Calcium carbonate	1.372	1.280	1.160
DL-Methionine	0.352	0.308	0.256
Natrium bicarbonate	0.204	0.212	0.136
Lysine-HCL 98	0.140	0.148	0.044
Salt	0.120	0.120	0.156
L-Threonine	0.044	0.040	0
Premix[1]	0.600	0.600	0.600
Analyzed chemical composition, g/kg dry matter (DM)			
DM	882	885	879
Crude protein	228	207	194
Crude fat	51.1	47.5	61.0
Crude fiber	28.0	29.0	30.1
Crude ash	52.6	50.0	46.3
Starch	356	388	401
Sugar	55.0	49.9	45.4
Calcium	8.88	8.39	7.63
Phosphorus	6.90	7.05	6.66
ME (MJ/kg)	12.0	12.0	12.4

[1]Provided per kilogram of complete starter diet (Garant - Tiernahrung GmbH, Pöchlarn, Austria): 12,500 IU of vitamin A, 5,000 IU of vitamin D_3, 75.0 mg of vitamin E, 6.0 mg of vitamin K3, 2.50 mg of vitamin B_1, 7.0 mg of vitamin B_2, 4.50 mg of vitamin B_6, 0.025 mg of vitamin B_{12}, 60.0 mg of nicotinic acid, 15.0 mg of pantothenic acid, 1.0 mg of folic acid, 0.25 mg of biotin, 1,582.065 mg of choline, 400.322 mg of choline chloride, 115.20 mg of betaine, 19.98 mg of ethoxyquin, 900.004 FTU of 6Phytase, 0.564 g of ß-glucan, 2.428 % of C 18:2, 2.804 % of polyenic acid, 30.059 mg of F-Xanto (total). Provided per kilogram of complete grower diet (Garant - Tiernahrung GmbH, Pöchlarn, Austria): 12,500 IU of vitamin A, 5,000 IU of vitamin D_3, 75.0 mg of vitamin E, 6.0 mg of vitamin K3, 2.50 mg of vitamin B_1, 7.0 mg of vitamin B_2, 4.50 mg of vitamin B_6, 0.025 mg of vitamin B_{12}, 60.0 mg of nicotinic acid, 15.0 mg of pantothenic acid, 1.0 mg of folic acid, 0.25 mg of biotin, 1,457.765 mg of choline, 400.322 mg of choline chloride, 115.20 mg of betaine, 19.98 mg of ethoxyquin, 900.004 FTU of 6Phytase, 0.618 g of ß-glucan, 2.692 % of C 18:2, 3.103% of polyenic acid, 30.866 mg of F-Xanto (total).

Provided per kilogram of complete finisher diet (Garant - Tiernahrung GmbH, Pöchlarn, Austria): 5,000 IU of vitamin D_3, 75.0 mg of vitamin E, 6.0 mg of vitamin K3, 2.50 mg of vitamin B_1, 7.0 mg of vitamin B_2, 4.5 mg of vitamin B_6, 0.025 mg of vitamin B_{12}, 60.0 mg of nicotinic acid, 15.0 mg of pantothenic acid, 1.0 mg of folic acid, 0.25 mg of biotin, 1,404.717 mg of choline, 400.322 mg of choline chloride, 115.20 mg of betaine, 19.98 mg of ethoxyquin, 900.004 FTU of 6Phytase, 0.639 g of ß-glucan, 3.098 % of C 18:2, 3.572 % of polyenic acid, 31.189 mg of F-Xanto (total).